<110> CuraGen Corporation et al. Alsobrook II, John Eichen, Joseph Lepley, Denise M. Miller, Charles E. Mezes, Peter Hahne, William

100

10/578234 IAP20 REC'UFCTIPTO 03 MAY 2006

<120> COMPOSITIONS AND METHODS OF USE FOR A FIBROBLAST GROWTH FACTOR <130> Cura-57 SNP <140> ***Enter Current Patent Application ID*** <141> 2004-11-3 <150> 10/702,126 <151> 2003-11-4 <160> 24 <170> CuraSeqList version 0.1 <210> 1 <211> 633 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(633) <400> 1 atg gct ccc tta gcc gaa gtc ggg ggc ttt ctg ggc ggc ctg gag ggc 48 Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu Gly Gly ttg ggc cag cag gtg ggt tcg cat ttc ctg ttg cct cct gcc ggg gag 96 Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu cgg ccg ccg ctg gtg ggc gag cgc agg agc gcg gcg gag cgg agc gcg 144 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala cgc ggc ggg ccg ggg gct gcg cag ctg gcg cac ctg cac ggc atc ctg 192 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu cgc cgc cgg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg 240 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu ccc gac ggc agc gtg cag ggc acc cgg cag gac cac agc ctc ttc ggt Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly 85 95 atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt 336 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly

gtg Val	gac Asp	agt Ser 115	ggt Gly	ctc Leu	tat Tyr	ctt Leu	gga Gly 120	atg Met	aat Asn	gac Asp	aaa Lys	gga Gly 125	gaa Glu	ctc Leu	tat Tyr	384
					act Thr											432
					acc Thr 150											480
					ttt Phe											528
					aag Lys											576
_			_		gaa Glu	_	-		_	_		_			_	624
_	tac Tyr 210															633
<21	0> 2 1> 2: 2> PI															
<21	3> H		sapi	ens												
<40	3> Ho 0> 2	omo s			Glu	Val	Gly	Gly	Phe 10	Leu	Gly	Gly	Leu	Glu 15	Gly	
<40 Met 1	3> Ho 0> 2 Ala	omo s	Leu	Ala 5 Val	Glu Gly				10			: .		15		
<40 Met 1 Leu	3> HG 0> 2 Ala Gly	Pro Gln	Leu Gln 20	Ala 5 Val		Ser	His	Phe 25	10 Leu	Leu	Pro	Pro	Ala 30	15 Gly	Glu	
<40 Met 1 Leu	3> HG 0> 2 Ala Gly Pro	Pro Gln Pro 35 Gly	Leu Gln 20 Leu	Ala 5 Val ; Leu	Gly	Ser Glu	His Arg	Phe 25 Arg	10 Leu Ser	Leu Ala	Pro	Pro Glu 45	Ala 30 Arg	15 Gly Ser	Glu Ala	
<400 Met 1 Leu Arg	3> He 0> 2 Ala Gly Pro Gly ,50 Arg	Pro Gln Pro 35	Gln 20 Leu Pro	Ala 5 Val ; Leu Gly	Gly	Ser Glu Ala 55	His Arg 40 Gln	Phe 25 Arg Leu	10 Leu Ser Ala	Leu Ala His	Pro Ala Leu 60	Pro Glu 45 His	Ala 30 Arg Gly	15 Gly Ser Ile	Glu Ala Leu	
<400 Met 1 Leu Arg Arg	3> He 0> 2 Ala Gly Pro Gly ,50 Arg	Pro Gln Pro 35 Gly Arg	Leu Gln 20 Leu Pro Gln	Ala 5 Val ; Leu Gly	Gly Gly Ala Tyr 70 Gln	Ser Glu Ala 55 Cys	His Arg 40 Gln	Phe 25 Arg Leu	10 Leu Ser Ala Gly	Leu Ala His Phe	Pro Ala Leu 60	Pro Glu 45 His	Ala 30 Arg Gly	15 Gly Ser Ile	Glu Ala Leu Leu 80	
<400 Met 1 Leu Arg Arg 65	3> HG 0> 2 Ala Gly Pro Gly ,50 Arg Asp	Pro Gln Pro 35 Gly Arg	Leu Gln 20 Leu Pro Gln Ser	Ala 5 Val ; Leu Gly Leu Val 85	Gly Gly Ala Tyr 70 Gln	Ser Glu Ala 55 Cys	His Arg 40 Gln Arg	Phe 25 Arg Leu Thr	10 Leu Ser Ala Gly Gln 90	Leu Ala His Phe 75 Asp	Pro Ala Leu 60 His	Pro Glu 45 His	Ala 30 Arg Gly Gln Leu	15 Gly Ser Ile Ile Phe 95	Glu Ala Leu Leu 80 Gly	
<400 Met 1 Leu Arg Arg 65 Pro	3> HG 0> 2 Ala Gly Pro Gly 50 Arg Asp	Pro Gln Pro 35 Gly Arg Gly Glu	Leu Gln 20 Leu Pro Gln Ser Phe 100 Gly	Ala 5 Val ; Leu Gly Leu Val 85	Gly Gly Ala Tyr 70 Gln Ser	Ser Glu Ala 55 Cys Gly Val	His Arg 40 Gln Arg Thr	Phe 25 Arg Leu Thr Arg Val 105	10 Leu Ser Ala Gly Gln 90 Gly	Leu Ala His Phe 75 Asp	Pro Ala Leu 60 His	Pro Glu 45 His Leu Ser	Ala 30 Arg Gly Gln Leu Ile 110	15 Gly Ser Ile Ile Phe 95 Arg	Glu Ala Leu Leu 80 Gly	

	130					135					140					
Glu 145	Asn	Trp	Tyr	Asn	Thr 150	Tyr	Ser	Ser	Asn	Ile 155	Tyr	Lys	His	Gly	Asp 160	
Thr	Gly	Arg	Arg	Tyr 165	Phe	Val	Ala	Leu	Asn 170	Lys	Asp	Gly	Thr	Pro 175	Arg	
Asp	Glý	Ala	Arg 180	Ser	Lys	Arg	His	Gln 185	Lys	Phe	Thr	His	Phe 190	Leu	Pro	
Arg	Pro	Val 195	Asp	Pro	Glu	Arg	Val 200	Pro	Glu	Leu	Tyr	Lys 205	Asn	Leu	Leu	
Met	Tyr 210	Thr														
<212	0> 3 1> 63 2> DN 3> Ho	IA	sapie	ens												
	0> 1> CI 2> (1		(633)	•												
atg	0> 3 gct Ala	ccc Pro	tta Leu	gcc Ala 5	gaa Glu	gtc Val	G1A G3G	ggc Gly	ttt Phe 10	ctg Leu	ggc Gly	ggc Gly	ctg Leu	gag Glu 15	ggc Gly	, 48
	ggc Gly															96
cgg Arg	ccg Pro	ccg Pro 35	ctg Leu	ctg Leu	ggc Gly	gag Glu	cgc Arg 40	agg Arg	agc Ser	gcg Ala	gcg Ala	gag Glu 45	cgg Arg	agc Ser	gcg Ala	144
	ggc Gly 50															192
	cgc Arg															240
	gac Asp															288
	ttg Leu															336
	gac Asp															384
gga	tca	gag	aaa	ctt	act	tcc	gaa	tgc	atc	ttt	agg	gag	cag	ttt	gaa	432

Gly	Ser 130	Glu	Lys	Leu	Thr	Ser 135	Glu	Cys	Ile	Phe	Arg 140	Glu	Gln	Phe	Glu	
gag Glu 145	aac Asn	tgg Trp	tat Tyr	aac Asn	acc Thr 150	tat Tyr	tca Ser	tct Ser	aac Asn	ata Ile 155	tat Tyr	aaa Lys	cat His	gga Gly	gac Asp 160	480
act Thr	ggc Gly	cgc Arg	agg Arg	tat Tyr 165	ttt Phe	gtg Val	gca Ala	ctt Leu	aac Asn 170	aaa Lys	gac Asp	gga Gly	act Thr	cca Pro 175	aga Arg	528
gat Asp	ggc Gly	gcc Ala	agg Arg 180	tcc Ser	aag Lys	agg Arg	cat His	cag Gln 185	aaa Lys	ttt Phe	aca Thr	cat His	ttc Phe 190	tta Leu	cct Pro	576
				cca Pro												624
_	tac Tyr 210															633
<21 <21	0> 4 1> 2: 2> Pi 3> He	RT	sapi	ens												
	0> 4 Ala	Pro	Leu	Ala 5	Glu	Val	Gly	Gly	Phe 10	Leu	Gly	Gly	Leu	Glu 15	Gly	
Leu	Gly	Gln	Gln 20	Val	Gly	Ser	His	Phe 25	Leu	Leu	Pro	Pro	Ala 30	Gly	Glu	
Arg	Pro	Pro 35		Leu	Gly	Glu	Arg 40	Arg	Ser	Ala	Ala	Glu 45	Arg	Ser	Ala	
Arg	Gly 50	_	Pro	Gly	Ala	Ala 55	Gln	Leu	Ala	His	Leu 60	His	Gly	Ile	Leu	,
Arg 65	_	Arg	Gln	Leu	Tyr 70	Cys	Arg	Thr	Gly	Phe 75	His	Leu	Gln	Ile	Leu 80	
Pro	Asp	Gly	Ser	Val 85	Gln	Gly	Thr	Arg	Gln 90	· Asp	His	Ser	Leu	Phe 95	Gly	
Ile	Leu	Glu	Phe 100	Ile	Ser	Val	Ala	Val 105	Gly	Leu	Val	Ser	Ile 110	Arg	Gly	
Val	Asp	Ser 115	_	Leu	Tyr	Leu	Gly 120		Asn	Asp	Lys	Gly 125	Glu	Leu	Tyr	
Gly	Ser 130		Lys	Leu	Thr	Ser 135		Cys	Ile	Phe	Arg 140		Gln	Phe	Glu	
Glu 145		Trp	Tyr	Asn	Thr 150		Ser	Ser	Asn	Ile 155		Lys	His	Gly	Asp 160	
Thr	Gly	/ Arg	arg	Tyr	Phe	Val	Ala	Leu	Asn	Lys	Asp	Gly	Thr	Pro	Arg	

165 170 175 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu 200 Met Tyr Thr 210 <210> 5 <211> 477 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(474) <400> 5 atg get cag etg get cae etg cat ggt ate etg egt ege egt cag etg Met Ala Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Gln Leu tac tgc cgt act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt 96 Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val 20 25 cag ggt acc cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile tct gtt gct gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg 192 Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu tac ctg ggt atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu acc tct gaa tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn 85 acc tac tct tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac 336 Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr 100 105 ttc qtt gct ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct 384 Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser 115 120 aaa cgt cac cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg 432 Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro 135 130 gag cgt gtt cca gaa ctg tat aaa aac ctg ctg atg tac acc taa 477 Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr 145 150

WO 2005/044991 PCT/US2004/036478 6/19

<210> 6 <211> 158 <212> PRT <213> Homo sapiens

<400> 6

Met Ala Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Gln Leu

Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val 30

Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile

Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu 55

Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu

Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn 85 90

Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr 100 105

Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser 120

Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro 130 135

Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr 145 150

<210> 7 <211> 540 <212> DNA <213> Homo sapiens

<220> <221> CDS <222> (1)..(537)

<400> 7

atg gct ccc tta gcc gaa gtc ggg ggc ttt ctg ggc ggc ctg gag ggc 48 Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu Glu Gly 1 5

ttg ggc cag ccg ggg gca gcg cag ctg gcg cac ctg cac ggc atc ctg 96 Leu Gly Gln Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu 20 30

ege ege egg cag ete tat tge ege ace gge tte cae etg eag ate etg 144 Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu 35 40

ccc gac ggc agc gcg cag ggc acc cgg cag gac cac agc ctc ttc ggt 192

Pro	Asp 50	Gly	Ser	Ala	Gln	Gly 55	Thr	Arg	Glr.	Asp	His		Let	ı Phe	∋ Gly	
ato Ile 65	ьeu	gaa Glu	ttc Phe	atc Ile	agt Ser 70	gtg Val	gca Ala	gtg Val	gga Gly	cto Leu 75	ı Val	agt Ser	att Ile	aga Arg	ggt Gly 80	240
gtg Val	gac Asp	agt Ser	ggt	ctc Leu 85	Tyr	ctt Leu	gga Gly	atg Met	aat Asn 90	Asp	aaa Lys	gga Gly	gaa Glu	cto Leu 95	tat Tyr	288
gga Gly	tca Ser	gag Glu	aaa Lys 100	ren	act Thr	tcc Ser	gaa Glu	tgc Cys 105	atc Ile	ttt Phe	agg Arg	gag Glu	cag Gln 110	Phe	gaa Glu	336
gag Glu	aac Asn	tgg Trp 115	Tyr	aac Asn	acc Thr	tat Tyr	tca Ser 120	Ser	aac Asn	ata Ile	tat Tyr	aaa Lys 125	cat His	gga Gly	gac Asp	384
act Thr	ggc Gly 130	cgc Arg	agg Arg	tat Tyr	ttt Phe	gtg Val 135	gca Ala	ctt Leu	aac Asn	aaa Lys	gac Asp 140	gga Gly	act Thr	cca Pro	aga Arg	432
gat Asp 145	ggc Gly	gcc Ala	agg Arg	tcc Ser	aag Lys 150	agg Arg	cat His	cag Gln	aaa Lys	ttt Phe 155	aca Thr	cat His	ttc Phe	tta Leu	cct Pro 160	480
aga Arg	cca Pro	gtg Val	gat Asp	cca Pro 165	gaa Glu	aga Arg	gtt Val	cca Pro	gaa Glu 170	ttg Leu	tac Tyr	aag Lys	aac Asn	cta Leu 175	ctg Leu	528
	tac Tyr		tag													540
<213 <213	0> 8 1> 1 ⁻ 2> PI 3> Ho	RT	sapie	ens												
<400 Met		Pro	Leu	Ala 5	Glu	Val	Gly	Gly	Phe 10	Leu	Gly	Gly	Leu	Glu 15	Gly	
Ļeu	Gly	Gln	Pro 20	Gly	Ala	Ala	Gln	Leu 25	Ala	His	Leu	His	Gly 30	Ile	Leu	
Arg	Arg	Arg 35	Gln	Leu	Tyr	Cys	Arg 40	Thr	Gly	Phe	His	Leu 45	Gln	Ile	Leu	
Pro	Asp 50	Gly	Ser	Ala	Gln	Gly 55	Thr	Arg	Gln	Asp	His 60	Ser	Leu	Phe	Gly	
Ile 65	Leu	Glu	Phe	Ile	Ser 70	Val	Ala	Val	Gly	Leu 75	Val	Ser	Ile	Arg	Gly 80	
Val	Asp	Ser	Gly	Leu 85	Tyr	Leu	Gly	Met	Asn 90	Asp	Lys	Gly	Glu	Leu 95	Tyr	
Gly	Ser	Glu	Lys	Leu	Thr	Ser	Glu	Cys	Ile	Phe	Arg	Glu	Gln	Phe	Glu	

```
100
                                105
                                                     110
Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
        115
                            120
                                                125
Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
                        135
Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
145
                    150
Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu
                165
                                    170
Met Tyr Thr
<210> 9
<211> 636
<212> DNA
<213> Homo sapiens
<400> 9
atggctccgc tggctgaagt tggtggtttc ctgggcggtc tggagggtct gggtcagcag 60
gttggttctc acttcctgct gccgccggct ggtgaacgtc cgccactgct gggtgaacgt 120
cgctccgcag ctgaacgctc cgctcgtggt ggcccgggtg ctgctcagct ggctcacctg 180
catggtatcc tgcgtcgccg tcagctgtac tgccgtactg gtttccacct gcagatcctg 240
ccggatggtt ctgttcaggg tacccgtcag gaccactctc tgttcggtat cctggaattc 300
atctctgttg ctgttggtct ggtttctatc cgtggtgttg actctggcct gtacctgggt 360
atgaacgaca aaggcgaact gtacggttct gaaaaactga cctctgaatg catcttccgt 420
gaacagtttg aagagaactg gtacaacacc tactcttcca acatctacaa acatggtgac 480
accggccgtc gctacttcgt tgctctgaac aaagacggta ccccgcgtga tggtgctcgt 540
tctaaacgtc accagaaatt cacccacttc ctgccgcgcc cagttgaccc ggagcgtgtt 600
ccagaactgt ataaaaacct gctgatgtac acctaa
<210> 10
<211> 540
<212> DNA
<213> Homo sapiens
<400> 10
atggctccct tagccgaagt cgggggcttt ctgggcggcc tggagggctt gggccagccg 60
ggggcagcgc agctggcgca cctgcacggc atcctgcgcc gccggcagct ctattgccgc 120
accggcttcc acctgcagat cctgcccgac ggcagcgtgc agggcacccg gcaggaccac 180
agcetetteg gtatettgga atteateagt gtggeagtgg gaetggteag tattagaggt 240
gtggacagtg gtctctatct tggaatgaat gacaaaggag aactctatgg atcagagaaa 300
cttacttccg aatgcatctt tagggagcag tttgaagaga actggtataa cacctattca 360
tetaacatat ataaacatgg agacactgge egeaggtatt ttqtqqcact taacaaagac 420
gqaactccaa gagatggcgc caggtccaag aggcatcaga aatttacaca tttcttacct 480
agaccagtgg atccagaaag agttccagaa ttgtacaaga acctactgat gtacacttag 540
<210> 11
<211> 179
<212> PRT
<213> Homo sapiens
<400> 11
Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu Glu Gly
```

Leu	Gly	Gln	Pro 20	Gly	Ala	Ala	Gln	Leu 25	Ala	His	Leu	His	Gly 30	Ile	Leu	
Arg	Arg	Arg 35	Gln	Leu	Tyr	Суѕ	Arg 40	Thr	Gly _.	Phe	His	Leu 45	Gln	Ile	Leu	
Pro	Asp 50	Gly	Ser	Val	Gln	Gly 55	Thr	Arg	Gln	Asp	His 60	Ser	Leu	Phe	Gly	
Ile 65	Leu	Glu	Phe	Ile	Ser 70	Val	Ala	Val	Gly	Leu 75	Val	Ser	Ile	Arg	Gly 80	
Val	Asp	Ser	Gly	Leu 85	Tyr	Leu	Gly	Met	Asn 90	Asp	Lys	Gly	Glu	Leu 95	Tyr	
Gly	Ser	Glu	Lys 100	Leu	Thr	Ser	Glu	Cys 105	Ile	Phe	Arg	Glu	Gln 110		Glu	
Glu	Asn	Trp 115	Tyr	Asn	Thr	Tyr	Ser 120	Ser	Asn	Ile	Tyr	Lys 125	His	Gly	Asp	
Thr	Gly 130	Arg	Arg	Tyr	Phe	Val 135	Ala	Leu	Asn	Lys	Asp 140	Gly	Thr	Pro	Arg	
Asp 145	Gly	Ala	Arg	Ser	Lys 150	Arg	His	Gln	Lys	Phe 155	Thr	His	Phe	Leu	Pro 160	
Arg	Pro	Val	Asp	Pro 165	Glu	Arg	Val	Pro	Glu 170	Leu	Tyr	Lys	Asn	Leu 175	Leu	
Met	Tyr	Thr														
<213 <213	0> 12 1> 63 2> DN 3> Ho	30 1A	sapie	ens												
	l> CI		(627)	ı												
)> 12															
ecg Pro 1	Leu	Ala	gaa Glu	Val 5	ggt Gly	ggt Gly	Phe	ctg Leu	ggc Gly 10	ggt Gly	ctg Leu	gag Glu	ggt Gly	ctg Leu 15	ggt Gly	48
cag Gln	cag Gln	gtt Val	ggt Gly 20	tct Ser	cac His	ttc Phe	ctg Leu	ctg Leu 25	ccg Pro	ccg Pro	gct Ala	ggt Gly	gaa Glu 30	cgt Arg	ccg Pro	96
cca Pro	ctg Leu	ctg Leu 35	ggt Gly	gaa Glu	cgt Arg	cgc Arg	tcc Ser 40	gca Ala	gct Ala	gaa Glu	cgc Arg	tcc Ser 45	gct Ala	cgt Arg	ggt Gly	144
ggc Gly	ccg Pro 50	ggt Gly	gct Ala	gct Ala	cag Gln	ctg Leu 55	gct Ala	cac His	ctg Leu	cat His	ggt Gly 60	atc Ile	ctg Leu	cgt Arg	cgc Arg	192
cgt	cag	ctg	tac	tgc	cqt	act	ggt	ttc	cac	cta	caσ	atc	cta	aca	αat	240

10/19

Arg 65	Gln	Leu	Tyr	Cys	Arg 70	Thr	Gly	Phe	His	Leu 75		Ile	Leu	Pro	Asp 80	
ggt Gly	tct Ser	gtt Val	cag Gln	ggt Gly 85	acc Thr	cgt Arg	cag Gln	gac Asp	cac His 90	Ser	ctg Leu	ttc Phe	ggt Gly	atc Ile 95	ctg Leu	288
gaa Glu	ttc Phe	atc Ile	tct Ser 100	gtt Val	gct Ala	gtt Val	ggt Glÿ	ctg Leu 105	gtt Val	tct Ser	atc Ile	cgt Arg	ggt Gly 110	gtt Val	gac Asp	336
tct Ser	ggc Gly	ctg Leu 115	tac Tyr	ctg Leu	ggt Gly	atg Met	aac Asn 120	gac Asp	aaa Lys	ggc Gly	gaa Glu	ctg Leu 125	tac Tyr	ggt Gly	tct Ser	384
gaa Glu	aaa Lys 130	ctg Leu	acc Thr	tct Ser	gaa Glu	tgc Cys 135	atc Ile	ttc Phe	cgt Arg	gaa Glu	cag Gln 140	ttt Phe	gaa Glu	gag Glu	aac Asn	432
tgg Trp 145	tac Tyr	aac Asn	acc Thr	tac Tyr	tct Ser 150	tcc Ser	aac Asn	atc Ile	tac Tyr	aaa Lys 155	cat His	ggt Gly	gac Asp	acc Thr	ggc Gly 160	480
cgt Arg	cgc Arg	tac Tyr	ttc Phe	gtt Val 165	gct Ala	ctg Leu	aac Asn	aaa Lys	gac Asp 170	ggt Gly	acc Thr	ccg Pro	cgt Arg	gat Asp 175	ggt Gly	528
gct Ala	cgt Arg	tct Ser	aaa Lys 180	cgt Arg	cac His	cag Gln	aaa Lys	ttc Phe 185	acc Thr	cac His	ttc Phe	ctg Leu	ccg Pro 190	cgc Arg	cca Pro	576
gtt Val	gac Asp	ccg Pro 195	gag Glu	cgt Arg	gtt Val	cca Pro	gaa Glu 200	ctg Leu	tat Tyr	aaa Lys	aac Asn	ctg Leu 205	ctg Leu	atg Met	tac Tyr	624
acc Thr	taa															630
<211 <212	0> 13 L> 20 2> PF B> Ho	9	apie	ens		-										
)> 13		Cl.	Wa l	C1	C1	Dh -	T	63	a 3	_			_		
1	пеа	мта	GIU	Val 5	СТĀ	стА	Pne	ьeu	10	GIY	Leu	Glu	Gly	Leu 15	Gly	
			20	Ser				25					30			
Pro	Leu	Leu 35	Gly	Glu	Arg	Arg	Ser 40	Ala	Ala	Glu	Arg	Ser 45	Ala	Arg	Gly	
Gly	Pro 50	Gly	Ala	Ala	Gln	Leu 55	Ala	His	Leu	His	Gly 60	Ile	Leu	Arg	Arg	
Arg 65	Gln	Leu	Tyr	Cys	Arg 70	Thr	Gly	Phe	His	Leu 75	Gln	Ile	Leu	Pro	Asp 80	

11/19 Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu 90 Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp 100 105 Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser 120 Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn 135 Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly . 150 155 Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly 170 Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro 180 185 Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr 200 Thr <210> 14 <211> 612 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(609) <400> 14 ggt ttc ctg ggc ggt ctg ggt ctg ggt cag gtt ggt tct cac 48 Gly Phe Leu Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His ttc ctg ctg ccg ccg gct ggt gaa cgt ccg cca ctg ctg ggt gaa cgt 96 Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln 144 40 ctg gct cac ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc cgt Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg 192 50 55 act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt acc 240 Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr 65 70

75

288

cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt gct

Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala

Val	ggt Gly	ctg Leu	gtt Val 100	tct Ser	atc Ile	cgt Arg	ggt Gly	gtt Val 105	gac Asp	tct Ser	ggc Gly	ctg Leu	tac Tyr 110	ctg Leu	ggt Gly	336
atg Met	aac Asn	gac Asp 115	aaa Lys	ggc Gly	gaa Glu	ctg Leu	tac Tyr 120	ggt Gly	tct Ser	gaa Glu	aaa Lys	ctg Leu 125	acc Thr	tct Ser	gaa Glu	384
tgc Cys	atc Ile 130	ttc Phe	cgt Arg	gaa Glu	cag Gln	ttt Phe 135	gaa Glu	gag Glu	aac Asn	tgg Trp	tac Tyr 140	aac Asn	acc Thr	tac Tyr	tct Ser	432
tcc Ser 145	aac Asn	atc Ile	tac Tyr	aaa Lys	cat His 150	ggt Gly	gac Asp	acc Thr	ggc Gly	cgt Arg 155	cgc Arg	tac Tyr	ttc Phe	gtt Val	gct Ala 160	480
ctg Leu	aac Asn	aaa Lys	gac Asp	ggt Gly 165	acc Thr	ccg Pro	cgt Arg	gat Asp	ggt Gly 170	gct Ala	cgt Arg	tct Ser	aaa Lys	cgt Arg 175	cac His	528
cag Gln	aaa Lys	ttc Phe	acc Thr 180	cac His	ttc Phe	ctg Leu	ccg Pro	cgc Arg 185	cca Pro	gtt Val	gac Asp	ccg Pro	gag Glu 190	cgt Arg	gtt Val	576
					aac Asn						taa					612
<211	0> 15 L> 20 2> PF)3														
	3> Ho		sapie	ens												
<213 <400	3> Ho 0> 15	omo s			Leu	Glu	Gly	Leu	Gly 10	Gln	Gln	Val	Gly	Ser 15	His	
<213 <400 Gly 1	3> Ho)> 15 Phe	omo s Leu	Gly	Gly 5	Leu Ala				10					15		
<213 <400 Gly 1 Phe	3> Ho)> 15 Phe Leu	omo s Leu Leu	Gly Pro 20	Gly 5 Pro		Gly	Glu	Arg 25	10 Pro	Pro	Leu	Leu	Gly 30	15 Glu	Arg	
<213 <400 Gly 1 Phe Arg	3> Ho D> 15 Phe Leu Ser	Leu Ala 35	Gly Pro 20 Ala	Gly 5 Pro Glu	Ala	Gly Ser	Glu Ala 40	Arg 25 Arg	10 Pro Gly	Pro Gly	Leu Pro	Leu Gly 45	Gly 30 Ala	15 Glu Ala	Arg Gln	
<213 <400 Gly 1 Phe Arg	3> Ho D> 15 Phe Leu Ser Ala 50	Leu Ala 35	Gly Pro 20 Ala	Gly 5 Pro Glu His	Ala Arg	Gly Ser Ile 55	Glu Ala 40 Leu	Arg 25 Arg Arg	10 Pro Gly Arg	Pro Gly Arg	Leu Pro Gln 60	Leu Gly 45 Leu	Gly 30 Ala Tyr	Glu Ala Cys	Arg Gln Arg	
<213 <400 Gly 1 Phe Arg Leu Thr 65	3> Ho D> 15 Phe Leu Ser Ala 50	Leu Ala 35 His	Gly Pro 20 Ala Leu His	Gly 5 Pro Glu His Leu	Ala Arg Gly	Gly Ser Ile 55 Ile	Glu Ala 40 Leu Leu	Arg 25 Arg Arg	10 Pro Gly Arg Asp	Pro Gly Arg Gly 75	Leu Pro Gln 60 Ser	Leu Gly 45 Leu Val	Gly 30 Ala Tyr	Glu Ala Cys Gly	Arg Gln Arg Thr 80	
<213 <400 Gly 1 Phe Arg Leu Thr 65 Arg	3> Ho Phe Leu Ser Ala 50 Gly	Leu Ala 35 His	Gly Pro 20 Ala Leu His	Gly 5 Pro Glu His Leu Ser 85	Ala Arg Gly Gln 70	Gly Ser Ile 55 Ile Phe	Glu Ala 40 Leu Leu Gly	Arg 25 Arg Arg Pro	10 Pro Gly Arg Asp Leu 90	Pro Gly Arg Gly 75 Glu	Leu Pro Gln 60 Ser	Leu Gly 45 Leu Val	Gly 30 Ala Tyr Gln	Glu Ala Cys Gly Val 95	Arg Gln Arg Thr 80 Ala	
<213 <400 Gly 1 Phe Arg Leu Thr 65 Arg Val	3> Ho Phe Leu Ser Ala 50 Gly Gln	Leu Ala 35 His Phe Asp	Gly Pro 20 Ala Leu His Val 100	Gly 5 Pro Glu His Leu Ser 85 Ser	Ala Arg Gly Gln 70 Leu	Gly Ser Ile 55 Ile Phe .	Glu Ala 40 Leu Leu Gly	Arg 25 Arg Arg Pro Ile Val 105	Pro Gly Arg Asp Leu 90 Asp	Pro Gly Arg Gly 75 Glu Ser	Leu Pro Gln 60 Ser Phe Gly	Leu Gly 45 Leu Val Ile	Gly 30 Ala Tyr Gln Ser Tyr 110	Glu Ala Cys Gly Val 95 Leu	Arg Gln Arg Thr 80 Ala	

13/19

130 135 140 Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His 165 170 Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val 180 Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr 200 <210> 16 <211> 603 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(600) <400> 16 ggc ggt ctg ggt ctg ggt cag cag gtt ggt tct cac ttc ctg ctg Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu ccg ccg gct ggt gaa cgt ccg cca ctg ctg ggt gaa cgt cgc tcc gca 96 Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala 25 gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct cag ctg gct cac Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His 35 ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc cgt act ggt ttc 192 Leu His Gly Ile Leu Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe 50 cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt acc cgt cag gac 240 His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp 65 cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt gct gtt ggt ctg 288 His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu 85 gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg ggt atg aac gac 336 Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp 100 aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct gaa tgc atc ttc 384 Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe 120 cgt gaa cag ttt gaa ġag aac tgg tac aac acc tac tct tcc aac atc 432 Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile 135

WO 2005/044991 PCT/US2004/036478

								14/1	9							
													ctg Leu			480
gac ,Asp													cag Gln			528
													cca Pro 190			576
			_	ctg Leu	_			taa								603
<211 <212)> 17 .> 20 ?> PF B> Ho	00 RT	sapie	ens												
)> 17 Gly		Glu	Gly 5	Leu	Gly	Gln	Gln	Val 10	Gly	Ser	His	Phe	Leu 15	Leu	
Pro	Pro	Ala	Gly 20	Glu	Arg	Pro	Pro	Leu 25	Leu	Gly	Glu	Arg	Arg 30	Ser	Ala	
Ala	Glu	Arg 35	Ser	Ala	Arg	Gly	Gly 40	Pro	Gly	Ala	Ala	Gln 45	Leu	Ala	His	
Leu	His 50	Gly	Ile	Leu	Arg	Arg 55	Arg	Gln	Leu	Tyr	Cys 60	Arg	Thr	Gly	Phe	
His 65	Leu	Gln	Ile	Leu	Pro 70	Asp	Gly	Ser	Val	Gln 75	Gly	Thr	Arg	Gln	Asp 80	
His	Ser	Leu	Phe	Gly 85	Ile	Leu	Glu	Phe	Ile 90	Ser	Val	Ala	Val	Gly 95	Leu	
Val	Ser	Ile	Arg 100	Gly	Val	Asp	Ser	Gly 105	Leu	Tyr	Leu	Gly	Met 110	Asn		
Lys	Gly	Glu 115	Leu	Tyr	Gly	Ser	Glu 120	Lys	Leu	Thr	Ser	Glu 125	Cys	Ile	Phe	
Arg	Glu 130	Gln	Phe	Glu	Glu	Asn 135	Trp	Tyr	Asn	Thr	Tyr 140	Ser	Ser	Asn	Ile	
Tyr 145	Lys	His	Gly	Asp	Thr 150	Gly	Arg	Arg	Tyr	Phe 155	Val	Ala	Leu	Asn	Lys 160	
Asp	Gly	Thr	Pro	Arg 165	Asp	Gly	Ala	Arg	Ser 170	Lys	Arg	His	Gln	Lys 175	Phe	
Thr	His	Phe	Leu 180		Arg	Pro	Val	Asp 185		Glu	Arg	Val	Pro 190	Glu	Leu	
Tyr	Lys	Asn 195		Leu	Met	Tyr	Thr									

<21 <21	.0> 1 .1> 5 .2> E	94 NA	sapi	ens												
	1> C		(591)												
gag	GTA	ctg	ggt Gly	cag Gln 5	Gln	gtt Val	ggt Gly	tct Ser	cac His	Phe	ctg Leu	ctg Leu	ccg Pro	ccg Pro	g gct Ala	48
ggt Gly	gaa Glu	cgt Arg	ccg Pro 20	Pro	ctg Leu	ctg Leu	ggt Gly	gaa Glu 25	cgt Arg	cgc Arg	tcc Ser	gca Ala	gct Ala 30	Glu	cgc Arg	96
tcc Ser	gct Ala	cgt Arg 35	GTA	ggc Gly	ccg Pro	ggt Gly	gct Ala 40	gct Ala	cag Gln	ctg Leu	gct Ala	cac His 45	ctg Leu	cat	ggt	144
atc Ile	ctg Leu 50	Arg	cgc Arg	cgt Arg	cag Gln	ctg Leu 55	Tyr	tgc Cys	cgt Arg	act Thr	ggt Gly 60	ttc Phe	cac His	ctg Leu	cag Gln	192
atc Ile 65	ctg Leu	ccg Pro	gat Asp	ggt Gly	tct Ser 70	gtt Val	cag Gln	ggt Gly	acc Thr	cgt Arg 75	cag Gln	gac Asp	cac His	tct Ser	ctg Leu 80	240
ttc Phe	ggt Gly	atc Ile	ctg Leu	gaa Glu 85	ttc Phe	atc Ile	tct Ser	gtt Val	gct Ala 90	gtt Val	ggt Gly	ctg Leu	gtt Val	tct Ser 95	atc Ile	288
cgt Arg	ggt Gly	gtt Val	gac Asp 100	tct Ser	ggc Gly	ctg Leu	tac Tyr	ctg Leu 105	ggt Gly	atg Met	aac Asn	gac Asp	aaa Lys 110	ggc Gly	gaa Glu	336
ctg Leu	tac Tyr	ggt Gly 115	tct Ser	gaa Glu	aaa Lys	ctg Leu	acc Thr 120	tct Ser	gaa Glu	tgc Cys	atc Ile	ttc Phe 125	cgt Arg	gaa Glu	cag Gln	384
ttt Phe	gaa Glu 130	gag Glu	aac Asn	tgg Trp	tac Tyr	aac Asn 135	acc Thr	tac Tyr	tct' Ser	tcc Ser	aac Asn 140	atc Ile	tac Tyr	aaa Lys	cat His	432
ggt Gly 145	gac Asp	acc Thr	ggc Gly	cgt Arg	cgc Arg 150	tac Tyr	ttc Phe	gtt Val	gct Ala	ctg Leu 155	aac Asn	aaa Lys	gac Asp	ggt Gly	acc Thr 160	480
ccg Pro	cgt Arg	gat Asp	ggt Gly	gct Ala 165	cgt Arg	tct Ser	aaa Lys	Arg	cac His 170	cag Gln	aaa Lys	ttc Phe	acc Thr	cac His 175	ttc Phe	528
ctg Leu	ccg Pro	cgc Arg	cca Pro 180	gtt Val	gac Asp	ccg Pro	gag Glu	cgt Arg 185	gtt Val	cca Pro	gaa Glu	ctg Leu	tat Tyr 190	aaa Lys	aac Asn	576
ctg	ctg	atg	tac	acc	taa											594

48

```
Leu Leu Met Tyr Thr
195
```

<210> 19

<211> 197

<212> PRT

<213> Homo sapiens

<400> 19

Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala 1 5 10 15

Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg $20 \hspace{1cm} 25 \hspace{1cm} 30$

Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly 35 40 45

Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln 50 55 60

Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu 65 70 75 80

Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile 85 90 95

Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu
100 105 110

Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln 115 120 125

Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His 130 135 140

Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr 145 150 155 160

Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe 165 170 175

Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn 180 185 190

Leu Leu Met Tyr Thr 195

<210> 20

<211> 567

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(564)

<400> 20

cac ttc ctg ctg ccg ccg gct ggt gaa cgt ccg cca ctg ctg ggt gaa His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu

1				5					10					15	i	
cgt Arg	cgc Arg	tcc Ser	gca Ala 20	gct Ala	gaa Glu	cgc Arg	tcc Ser	gct Ala 25	cgt Arg	ggt	ggc Gly	ccg Pro	ggt Gly 30	Ala	gct Ala	96
cag Gln	ctg Leu	gct Ala 35	cac His	ctg Leu	cat His	ggt Gly	atc Ile 40	ctg Leu	cgt Arg	cgc Arg	cgt Arg	cag Gln 45	ctg Leu	tac Tyr	tgc Cys	144
cgt Arg	act Thr 50	ggt Gly	ttc Phe	cac His	ctg Leu	cag Gln 55	atc	ctg Leu	ccg Pro	gat Asp	ggt Gly 60	tct Ser	gtt Val	cag Gln	ggt Gly	192
acc Thr 65	cgt Arg	cag Gln	gac Asp	cac His	tct Ser 70	ctg Leu	ttc Phe	ggt Gly	atc Ile	ctg Leu 75	gaa Glu	ttc Phe	atc Ile	tct Ser	gtt Val 80	240
gct Ala	gtt Val	ggt Gly	ctg Leu	gtt Val 85	tct Ser	atc Ile	cgt Arg	ggt Gly	gtt Val 90	gac Asp	tct Ser	ggc	ctg Leu	tac Tyr 95	ctg Leu	288
ggt Gly	atg Met	aac Asn	gac Asp 100	aaa Lys	ggc Gly	gaa Glu	ctg Leu	tac Tyr 105	ggt Gly	tct Ser	gaa Glu	aaa Lys	ctg Leu 110	acc Thr	tct Ser	336
gaa Glu	tgc Cys	atc Ile 115	ttc Phe	cgt Arg	gaa Glu	cag Gln	ttt Phe 120	gaa Glu	gag Glu	aac Asn	tgg Trp	tac Tyr 125	aac Asn	acc Thr	tac Tyr	384
tct Ser	tcc Ser 130	aac Asn	atc Ile	tac Tyr	aaa Lys	cat His 135	ggt Gly	gac Asp	acc Thr	ggc Gly	cgt Arg 140	cgc Arg	tac Tyr	ttc Phe	gtt Val	432
gct Ala 145	ctg Leu	aac Asn	aaa Lys	gac Asp	ggt Gly 150	acc Thr	ccg Pro	cgt Arg	gat Asp	ggt Gly 155	gct Ala	cgt Arg	tct Ser	aaa Lys	cgt Arg 160	480
cac His	cag Gln	aaa Lys	ttc Phe	acc Thr 165	cac His	ttc Phe	ctg Leu	ccg Pro	cgc Arg 170	cca Pro	gtt Val	gac Asp	ccg Pro	gag Glu 175	cgt Arg	528
gtt Val	cca Pro	Glu	ctg Leu 180	tat Tyr	aaa Lys	aac Asn	ctg Leu	ctg Leu 185	atg Met	tac Tyr	acc Thr	taa				567
<211 <212	> 21 > 18 > PR > Ho	8 T	apie	ens												
	> 21 Phe		Leu	Pro 5	Pro	Ala	Gly	Glu	Arg 10	Pro	Pro	Leu	Leu	Gly 15	Glu	
Arg	Arg	Ser	Ala 20	Ala	Glu	Arg	Ser	Ala 25	Arg	Gly	Gly	Pro	Gly 30	Ala	Ala	
Gln	Leu	Ala 35	His	Leu	His	Gly	Ile 40	Leu	Arg	Arg	Arg	Gln 45	Leu	Tyr	Cys	

. .

Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly 50 55 60

Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val 65 70 75 80

Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu 85 90 95 ·

Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser 100 105 110

Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr 115 120 125

Ser Ser Asn Ile Tyr Lys His Gly A'sp Thr Gly Arg Arg Tyr Phe Val 130 135 140

Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg 145 150 155 160

His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg 165 170 175

Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr 180 185

<210> 22

<211> 447

<212> DNA

<213> Homo sapiens

<400> 22

atcetgegee geeggeaget etattgeege aceggettee acetgeagat cetgeegae 60 ggeaggetge agggeaceeg geaggaceae ageetetteg gtatettgga atteateagt 120 gtggeagtgg gaetggteag tattagaggt gtggacagtg gtetetatet tggaatgaat 180 gacaaaggag aactetatgg atcagagaaa ettactteeg aatgeatett tagggageag 240 tttgaagga actggtataa cacetattea tetaacatat ataaacatgg agacactgge 300 egeaggtatt ttgtggeaet taacaaagae ggaacteeaa gagatggege caggteeaag 360 aggeateaga aatttacaca tttettacet agaceagtgg atceagaaa agtteeagaa 420 ttgtacaagg acetactgat gtacact

₹210> 23

<211> 149

<212> PRT

<213> Homo sapiens

<400> 23

Ile Leu Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln
1 5 10 15

Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu 20 25 30

Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile 35 40 45

Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu 50 55 60

```
Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln
                     70
Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His
Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr
Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe
        115
                            120
Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn
                        135
Leu Leu Met Tyr Thr
145
<210> 24
<211> 537
<212> DNA
<213> Homo sapiens
<400> 24
atggeteect tageegaagt egggggettt etgggeggee tggagggett gggeeageeg 60
ggggcagcgc agctggcgca cctgcacggc atcctgcgcc gccggcagct ctattgccgc 120
accggettee acctgeagat cetgeeegae ggeagegtge agggeaeeeg geaggaeeae 180
agcctcttcg gtatcttgga attcatcagt gtggcagtgg gactggtcag tattagaggt 240
gtggacagtg gtctctatct tggaatgaat gacaaaggaq aactctatqq atcaqaqaaa 300
cttacttccg aatgcatctt tagggagcag tttgaagaga actggtataa cacctattca 360
tctaacatat ataaacatgg agacactggc cgcaggtatt ttgtggcact taacaaagac 420
ggaactccaa gagatggcgc caggtccaag aggcatcaga aatttacaca tttcttacct 480
agaccagtgg atccagaaag agttccagaa ttgtacaaga acctactgat gtacact
```

TRA 1973383v1